

**This Page Is Inserted by IFW Operations
and is not a part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- **BLACK BORDERS**
- **TEXT CUT OFF AT TOP, BOTTOM OR SIDES**
- **FADED TEXT**
- **ILLEGIBLE TEXT**
- **SKEWED/SLANTED IMAGES**
- **COLORED PHOTOS**
- **BLACK OR VERY BLACK AND WHITE DARK PHOTOS**
- **GRAY SCALE DOCUMENTS**

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

FIG. 1

Multiple Alignment:

Multiple Alignment:

SPI	SPkinaseinHSDA59H18	MEKPYAFTVHCVKRAARRHRWKWAQVTFWCPEEQCHLWLQTLREMLEKLTSEPKHLLVFI
CA	CAB62977	-----PKHLLVFI
SPI	SPkinaseinHSDA59H18	NPFGGKGQGKRIYERKVAFLFTLASITTDIGNKFFVN YVEVITEHANQAKETLYEINID
CA	CAB62977	NPFGGKGQGKRIYERKVAFLFTLASITTDIGNKFFVN YVEVITEHANQAKETLYEINID
SPI	SPkinaseinHSDA59H18	KYDGI VCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPR A VLPSSLRIGIIPAGSTDCWCY
CA	CAB62977	KYDGI VCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPR A VLPSSLRIGIIPAGSTDCWCY
SPI	SPkinaseinHSDA59H18	STVGTSDAETSA LHI VVGDSLAMDVSS VHHNSTLLEY S VSLG YGFYGD I IKDSEKKRWL
CA	CAB62977	STVGTSDAETSA LHI VVGDSLAMDVSS VHHNSTLLEY S VSLG YGFYGD I IKDSEKKRWL
SPI	SPkinaseinHSDA59H18	GLARYDFSGLKTF LSHHCYEGT VSFLPAQHTVGSPEDEKPCRAGCFVCRQSKQQL EEEQK
CA	CAB62977	GLARYDFSGLKTF LSHHCYEGT VSFLPAQHTVGSPEDEKPCRAGCFVCRQSKQQL EEEQK
SPI	SPkinaseinHSDA59H18	KALYGLEAAEDVEEWQVVCCKFLAINATNMSCACRRS PRGLSPA AHLGDGSSDLILIRKC
CA	CAB62977	KALYGLEAAEDVEEWQVVCCKFLAINATNMSCACRRS PRGLSPA AHLGDGSSDLILIRKC
SPI	SPkinaseinHSDA59H18	SSEFNFLRLIEHTNQDQDFTFVEVYRVKKFQFTSKHMEDESDLKEGGKKRFGHICSS
CA	CAB62977	SSEFNFLRLIEHTNQDQD-----
SPI	SPkinaseinHSDA59H18	HPSCCCTVSNSWNCDGEVLHSPAIEVRVHCQLVRLFARGIEENPKPDSHS
CA	CAB62977	-----

FIG. 2

Multiple Alignment:

```

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  PKHLLVF INPFGKGQGR IYERKVAPLFTLASITTD IIGNKFYVNYVEVITEHANQAKE

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  TLYEINI DKYDGI VCVGGDGMFSEVLHGLIGRTQRSAGVDQNHPRAVLPSSLRIGIIPA

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  GSTDCVCYSTVGTSDAETSA LHI VVGDS LAMDVSSVHHNSTLLRYSVSLG YGFYGD I IK

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  DSEKKRWLGLARYDFSGLK TFLSHHCYEGTVSFLPAQHTVGSPDRDKPCRAGCFVCRQSK

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  QQLEEEQKKALYGLEAAEDV EEWQVVC GKFLA INA INMSCACAPESPGELSPFAHLGDGSS
                    FLA IN INMSCACAPESPGELSPFAHLGDGSS

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  DLILIRKCSRNFLEFLIRHTNQEDQFGFTFVEVYRVKKFQFTSKHVEDDNDLKELEKQ
                    DLILIRKCSRNFLEFLIRHTNQDQFDFTFVEVYRVKKFQFTSKHVEDDNDLKEGGRK

S2180312      -----
A1237625      -----
SPkinaseinHSDA59H18  KFGKICKDRPSCCTCSASRSWN CDGEVWHSP AIEVRVHCQLVLFARGIEEES
                    KFGQICKDNPPCACTSRSSWN CDGEVLHSP AIEVRVHCQLVLFARGIEEES
                    KFGHICSSHPSCCTVSNSSWN CDGEVLHSP AIEVRVHCQLVLFARGIEENPKPDSHS

```


FIG. 4

PHYLIP - Protein Distance Analysis

Sequences analyzed:

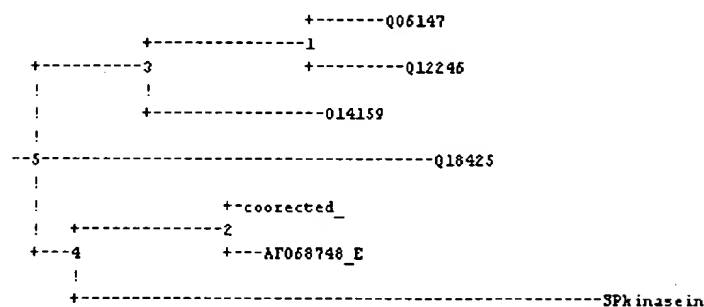
1. SPkinaseinHSDA59H18
2. Q18425
3. O14159
4. Q06147
5. Q12246
6. coorrected_human_sphingosine
7. AF068748_EXT-2

7 Populations

Neighbor-Joining/UPGMA method version 3.572c

Neighbor-joining method

Negative branch lengths allowed



remember: this is an unrooted tree!

Between	And	Length
5	3	1.09970
3	1	1.59865
1	Q06147	0.79847
1	Q12246	1.02742
3	Q14159	1.74537
5	Q18425	4.00995
5	4	0.43259
4	2	1.44382
2	coorrected_	0.24774
2	AF068748_E	0.37392
4	SPkinasein	5.26443

FIG. 5

Multiple Alignment:

80432911 SPkinaseinHSDA59H18	AGAPGADAGSVVSEIIAVEETDVHGKHQSGKWKQIMKPYAFTVHCVKRA RHRWKWAQ -----MEKPYAFTVHCVKRA RHRWKWAQ
80432911 SPkinaseinHSDA59H18	WTFWCPEEQCHLWLQTLREMLEKLTSPKHL VFINPFGKGQGKERIYERKVAPLFTLA WTFWCPEEQCHLWLQTLREMLEKLTSPKHL VFINPFGKGQGKERIYERKVAPLFTLA
80432911 SPkinaseinHSDA59H18	SITTDI I-----TEHANQAKETLVEINIDKYDGIWCVGGDGMFSEVLHGLIGR SITTDIIGNKFFWN YVEWTEHANQAKETLVEINIDKYDGIWCVGGDGMFSEVLHGLIGR
80432911 SPkinaseinHSDA59H18	TQESAGVDQNHPR----- TQESAGVDQNHPR A VLPSSLRIGIIPAGSTDCV CYSTVGTSDAETSALHIWGD SLAMD
80432911 SPkinaseinHSDA59H18	WSSVHHNSTLLRYSVLLGYGYGDI IKDSEKKRWGLARYDFSGLKTF LSHHCYEGTVS -----
80432911 SPkinaseinHSDA59H18	FLPAQHTVGS PRDEKPCRAGCFVCRQSKQQL EEQKKALYGLEAAEDVEEWQWVCGKFLA -----
80432911 SPkinaseinHSDA59H18	INATNMSCACRES PRGLSPAHLGDGSSDL ILIRKCSRNFLEFLIRHTNQDQDFTFV -----
80432911 SPkinaseinHSDA59H18	EYERVKKEFQFTSKHMEDESD LKEGGHRRFGHICSSHPSCCCTVSNSSWNICDGEVLH3PA -----
80432911 SPkinaseinHSDA59H18	IEVEVHCQVRLFA RGI EENPEPDSHS -----